

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 23, 2002, 02:21:48 ; Search time 312 Seconds

(without alignments)
151.577 Million cell updates/sec

Title: US-09-805-761-34

Perfect score: 21

Sequence: 1 ugcttgagatgtactgcau 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 2331924

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- N_Geneseq_101002.*
- 1: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
 - 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
 - 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
 - 4: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
 - 5: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
 - 6: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
 - 7: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
 - 8: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
 - 9: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
 - 10: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
 - 11: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
 - 12: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
 - 13: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
 - 14: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
 - 15: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
 - 16: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
 - 17: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
 - 18: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
 - 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
 - 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
 - 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
 - 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
 - 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
 - 24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	AAI64166	Vascular endothelial
2	21	100.0	21	AAH22984	VEGF specific anti
3	21	100.0	21	AAH23027	VEGF specific anti
4	21	100.0	21	AAH23032	VEGF gene fragment
5	21	100.0	21	AAH23033	VEGF- α gene fragment
6	21	100.0	21	AAH23035	Human VEGF gene fr
7	21	100.0	21	AAH23040	VEGF expression in
8	21	100.0	33	AAH23010	Antisense sequence
9	21	100.0	42	AAT10126	

10	21	100.0	48	22	AAI12814	Human VEGF-A rever
11	21	100.0	62	22	AAH23029	VEGF-A gene fragme
12	20	95.2	20	22	AAH23005	VEGF expression in
13	20	95.2	20	22	AAH23008	VEGF expression in
14	20	95.2	21	22	AAH22998	VEGF expression in
15	20	95.2	21	22	AAH22999	VEGF expression in
16	19.4	92.4	21	22	AAH23025	VEGF expression in
17	19	90.5	19	22	AAH23006	VEGF expression in
18	19	90.5	19	22	AAH23009	VEGF expression in
19	19	90.5	21	22	AAH22997	VEGF expression in
20	18.4	87.6	21	22	AAH23041	Mouse VEGF gene fr
21	18	85.7	18	22	AAH23007	VEGF expression in
22	18	85.7	21	22	AAH22996	VEGF expression in
23	18	85.7	21	22	AAH23001	VEGF expression in
24	17.8	84.8	21	22	AAH23024	VEGF expression in
25	17.8	84.8	21	22	AAH23026	VEGF expression in
26	17	81.0	20	22	AAH23002	VEGF expression in
27	16	76.2	16	21	AAH23003	Immunosuppressant
28	16	76.2	19	22	AAH23003	VEGF expression in
29	16	76.2	19	22	AAH23003	VEGF hammerhead r
30	15.4	73.3	21	22	AAH22995	Human CXAX process
31	15.2	72.4	27	20	AAV84250	Mutant vascular en
32	15.2	72.4	36	17	AAT31261	Immunosuppressant
33	15.2	71.4	16	21	AAZ65573	VEGF expression in
34	15	71.4	18	22	AAH23004	Sequence antisense
35	15	71.4	20	19	AAT95395	VEGF expression in
36	15	71.4	21	22	AAH22993	Human lung tumour
37	14.8	70.5	24	24	ABL49258	Human spliced tran
38	14.6	69.5	60	24	ABN33027	VEGF expression in
39	14.4	68.6	21	22	AAH22994	Human CXAX process
40	14.2	67.6	27	20	AAV84251	Candida lusitanae
41	14.2	67.6	39	22	AAH02122	Mouse spliced tran
42	14.2	67.6	65	24	ABN52558	Immunosuppressant
43	14.2	66.7	18	14	AAZ65594	Human multi drug r
44	14	66.7	19	22	AAF91081	
45	14	66.7	19	22	AAF91081	

ALIGNMENTS

RESULT 1
AAI64166
ID AAI64166 standard; DNA; 21 BP.
XX AAI64166;
AC AAI64166;
XX 22-JAN-2002 (first entry)
DT Vascular endothelial growth factor antisense oligonucleotide (Veglin-3).
DE Vascular endothelial growth factor; VEGF; cytostatic; anti-HIV;
XX Vascular endothelial growth factor; VEGF; cytostatic; anti-HIV;
KW anti-inflammatory; immunosuppressive; antiproliferative; VEGF inhibitor;
KW Kaposi's sarcoma; vascular proliferation; cancer; antisense; tumour;
KW proliferative retinal disease; rheumatoid arthritis; lupus erythematosus;
KW psoriasis; pemphigus; proliferative retinopathy; diabetes mellitus; ss.
OS Homo sapiens.
XX
XX US6291667-B1.
XX
XX 18-SEP-2001.
XX
XX 30-JAN-1998; 98US-0016541.
XX
XX 31-JAN-1997; 97US-037004P.
XX
XX (GILL/) GILL P. S.
PA (MASO/) MASOOD R.
XX
XX Gill PS, Masood R;
XX WPI; 2001-637975/73.
DR

XX PT New vascular endothelial growth factor antisense oligonucleotides,
 PT useful for treating Kaposi's sarcoma, and diseases associated with
 PS vascular proliferation, e.g. cancer, proliferative retinal diseases.
 PS Claim 1; Column 13; 22pp; English.
 XX CC The present sequence represents a vascular endothelial growth factor
 CC (VEGF) antisense oligonucleotide, designated Veglin-3. The specification
 CC describes two new VEGF antisense oligonucleotides. The invention relates
 CC to the pharmacological use of VEGF inhibitor antisense oligonucleotides
 CC in the treatment of Kaposi's sarcoma. The oligonucleotides have
 CC cytostatic, anti-HIV, anti-inflammatory, immunosuppressive and
 CC antiproliferative activities. The antisense oligonucleotides act as VEGF
 CC inhibitors. The VEGF antisense oligonucleotides are not only useful for
 CC treating Kaposi's sarcoma but other diseases in which vascular
 CC proliferation plays a role e.g. cancer, proliferative retinal diseases or
 CC collagen vascular diseases (e.g. rheumatoid arthritis, lupus
 CC erythematosus, psoriasis and pemphigus). The oligonucleotides can be
 CC further used in the treatment of pre-cancerous conditions, solid tumours,
 CC proliferative retinopathy, and proliferative angiodysplasias of diabetes
 CC mellitus.
 XX CC Sequence 21 BP; 5 A; 3 C; 6 G; 7 T; 0 other;

Query Match 100.0%; Score 21; DB 22; Length 21;
 Best Local Similarity 90.5%; Pred. No. 0.76;
 Matches 19; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 UGGCTTGAAGATGTACTCGAT 21
 Db 1 TGGCTTGAAGATGTACTCGAT 21

RESULT 2

AAH22984
 ID AAH22984 standard; DNA; 21 BP.

AC AAH22984;
 DT 17-SEP-2001 (first entry)
 DE VEGF specific antisense oligo Veglin-3.

XX Vascular endothelial growth factor; VEGF; antisense; angiogenesis;
 KW cell proliferation; Kaposi's sarcoma; cancer; melanoma; cytostatic;
 KW antisense therapy; ss.

OS Synthetic.
 OS Homo sapiens.
 PN WO200152904-A2.

XX 26-JUL-2001.
 PD 19-JAN-2001; 2001WO-US000019.
 XX 19-JAN-2000; 2000US-0487023.

PR 19-JAN-2000; 2000US-0487023.
 XX (GILL/) GILL P S.
 PA Gill PS, Masood R;
 DR WPI; 2001-451898/48.

XX Novel antisense oligonucleotides useful for inhibiting vascular
 PT endothelial growth factor expression, angiogenesis and for treating
 PT cancer, e.g., Kaposi's sarcoma, ovarian cancer and prostate cancer
 XX Claim 10; Page 16; 105pp; English.

XX The invention provides a composition comprising one or more antisense
 CC oligonucleotides directed against vascular endothelial growth factor

CC (VEGF) where the antisense oligonucleotides inhibits proliferation of
 CC cells exhibiting autocrine VEGF activity at an IC₅₀ concentration of
 CC between 0.5-2.5 micro Ma. The antisense oligonucleotides may be directed
 CC against VEGF for inhibiting cancer cell proliferation and angiogenesis.
 CC Preferably the oligonucleotide AAH23032 (a modified version of AAH22984)
 CC is used and may be utilized to treat Kaposi's sarcoma, ovarian cancer,
 CC prostate cancer, pancreatic cancer or melanoma. The present sequence
 XX represents an antisense oligonucleotide directed against VEGF.

Sequence 21 BP; 5 A; 3 C; 6 G; 7 T; 0 other;

Query Match 100.0%; Score 21; DB 22; Length 21;
 Best Local Similarity 90.5%; Pred. No. 0.76;
 Matches 19; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGCTTGAAGATGTACTCGAT 21
 Db 1 TGGCTTGAAGATGTACTCGAT 21

RESULT 3

AAH23027
 ID AAH23027 standard; DNA; 21 BP.

XX AAH23027;
 DT 17-SEP-2001 (first entry)
 DE VEGF specific antisense oligo AS-3 mixed backbone derivative.

XX Vascular endothelial growth factor; VEGF; antisense; angiogenesis;
 KW cell proliferation; Kaposi's sarcoma; cancer; melanoma; cytostatic;
 KW antisense therapy; ss.

OS Synthetic.
 OS Homo sapiens.
 PN WO200152904-A2.

XX 26-JUL-2001.
 PD 19-JAN-2001; 2001WO-US000019.
 XX 19-JAN-2000; 2000US-0487023.

PR (GILL/) GILL P S.
 PA Gill PS, Masood R;
 DR WPI; 2001-451898/48.

XX Novel antisense oligonucleotides useful for inhibiting vascular
 PT endothelial growth factor expression, angiogenesis and for treating
 PT cancer, e.g., Kaposi's sarcoma, ovarian cancer and prostate cancer
 XX Example 13; Page 57; 105pp; English.

XX The invention provides a composition comprising one or more antisense
 CC oligonucleotides directed against vascular endothelial growth factor
 CC (VEGF) where the antisense oligonucleotides inhibits proliferation of
 CC cells exhibiting autocrine VEGF activity at an IC₅₀ concentration of
 CC between 0.5-2.5 micro Ma. The antisense oligonucleotides may be directed
 CC against VEGF for inhibiting cancer cell proliferation and angiogenesis.
 CC Preferably the oligonucleotide AAH23032 (a modified version of AAH22984)
 CC is used and may be utilized to treat Kaposi's sarcoma, ovarian cancer,
 CC prostate cancer, pancreatic cancer or melanoma. The present sequence
 CC represents a mixed backbone derivative of an antisense oligonucleotide
 CC AS-3 directed against VEGF.

Sequence 21 BP; 5 A; 3 C; 6 G; 5 T; 2 U; 0 other;

Query Match 100.0%; Score 21; DB 22; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.76;

XX 19-JAN-2000; 2000US-0487023.
 XX (GILL/) GILL P S.
 XX Gill PS, Masood R;
 XX WPI; 2001-451898/48.
 XX Novel antisense oligonucleotides useful for inhibiting vascular
 PT endothelial growth factor expression, angiogenesis and for treating
 PT cancer, e.g., Kaposi's sarcoma, ovarian cancer and prostrate cancer
 XX Examples; Fig 17b; 105pp; English.

XX The invention provides a composition comprising one or more antisense
 CC oligonucleotides directed against vascular endothelial growth factor
 CC (VEGF) where the antisense oligonucleotides inhibits proliferation of
 CC cells exhibiting autocrine VEGF activity at an IC₅₀ concentration of
 CC between 0.5-2.5 micro Ma. The antisense oligonucleotides may be directed
 CC against VEGF for inhibiting cancer cell proliferation and angiogenesis.
 CC Preferably the oligonucleotide AAH23032 (a modified version of AAH22984)
 CC is used and may be utilized to treat Kaposi's sarcoma, ovarian cancer,
 CC prostrate cancer, pancreatic cancer or melanoma. The present sequence
 CC represents a VEGF-A gene fragment.

XX Sequence 21 BP; 7 A; 6 C; 3 G; 5 T; 0 other;
 SQ

Query Match 100.0%; Score 21; DB 22; Length 21;
 Best Local Similarity 90.5%; Pred. No. 0.76;
 Matches 19; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UGGCTTGAAGATGACTCGAU 21
 Db 21 TGGCTTGAAGATGACTCGAT 1

RESULT 7
 AAH23040/c
 ID AAH23040 standard; DNA; 21 BP.
 AC AAH23040;
 DT 17-SEP-2001 (first entry)
 DE Human VEGF gene fragment complementary to AS-3m antisense oligo.
 DE Vascular endothelial growth factor; VEGF; antisense; angiogenesis;
 KW cell proliferation; Kaposi's sarcoma; cancer; melanoma; cytostatic;
 KW antisense therapy; ds.
 XX Homo sapiens.
 OS WO200152904-A2.
 PN 26-JUL-2001.
 PD 19-JAN-2001; 2001WO-US00019.
 PF 19-JAN-2000; 2000US-0487023.
 PR (GILL/) GILL P S.
 PA Gill PS, Masood R;
 XX WPI; 2001-451898/48.
 XX Novel antisense oligonucleotides useful for inhibiting vascular
 PT endothelial growth factor expression, angiogenesis and for treating
 PT cancer, e.g., Kaposi's sarcoma, ovarian cancer and prostrate cancer
 XX Examples; Fig 17c; 105pp; English.

CC The invention provides a composition comprising one or more antisense
 CC oligonucleotides directed against vascular endothelial growth factor
 CC (VEGF) where the antisense oligonucleotides inhibits proliferation of
 CC cells exhibiting autocrine VEGF activity at an IC₅₀ concentration of
 CC between 0.5-2.5 micro Ma. The antisense oligonucleotides may be directed
 CC against VEGF for inhibiting cancer cell proliferation and angiogenesis.
 CC Preferably the oligonucleotide AAH23032 (a modified version of AAH22984)
 CC is used and may be utilized to treat Kaposi's sarcoma, ovarian cancer,
 CC prostrate cancer, pancreatic cancer or melanoma. The present sequence
 CC represents a human VEGF gene fragment complementary to AS-3m antisense
 CC oligo.

XX Sequence 21 BP; 7 A; 6 C; 3 G; 5 T; 0 other;
 SQ

Query Match 100.0%; Score 21; DB 22; Length 21;
 Best Local Similarity 90.5%; Pred. No. 0.76;
 Matches 19; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UGGCTTGAAGATGACTCGAU 21
 Db 21 TGGCTTGAAGATGACTCGAT 1

RESULT 8
 AAH23010
 ID AAH23010 standard; DNA; 33 BP.
 AC AAH23010;
 DT 17-SEP-2001 (first entry)
 DE VEGF expression inhibiting antisense oligo.
 DE Vascular endothelial growth factor; VEGF; antisense; angiogenesis;
 KW cell proliferation; Kaposi's sarcoma; cancer; melanoma; cytostatic;
 KW antisense therapy; ss.
 XX Synthetic.
 OS Homo sapiens.
 PN WO200152904-A2.
 PD 26-JUL-2001.
 PF 19-JAN-2001; 2001WO-US00019.
 PR 19-JAN-2000; 2000US-0487023.
 PA (GILL/) GILL P S.
 XX Gill PS, Masood R;
 PI WPI; 2001-451898/48.
 DR Novel antisense oligonucleotides useful for inhibiting vascular
 XX endothelial growth factor expression, angiogenesis and for treating
 PT cancer, e.g., Kaposi's sarcoma, ovarian cancer and prostrate cancer
 XX Claim 3; Page 52; 105pp; English.

XX The invention provides a composition comprising one or more antisense
 CC oligonucleotides directed against vascular endothelial growth factor
 CC (VEGF) where the antisense oligonucleotides inhibits proliferation of
 CC cells exhibiting autocrine VEGF activity at an IC₅₀ concentration of
 CC between 0.5-2.5 micro Ma. The antisense oligonucleotides may be directed
 CC against VEGF for inhibiting cancer cell proliferation and angiogenesis.
 CC Preferably the oligonucleotide AAH23032 (a modified version of AAH22984)
 CC is used and may be utilized to treat Kaposi's sarcoma, ovarian cancer,
 CC prostrate cancer, pancreatic cancer or melanoma. Sequences AAH22985-23011
 CC represent antisense oligonucleotides directed against VEGF.

XX Sequence 33 BP; 9 A; 6 C; 11 G; 7 T; 0 other;
 SQ

XX PN WO200152904-A2.
 XX PD 26-JUL-2001.
 XX PF 19-JAN-2001; 2001WO-US00019.
 XX PR 19-JAN-2000; 2000US-0487023.
 XX PA (GILL/) GILL P S.
 XX PI Gill PS, Masood R;
 XX DR WPI; 2001-451898/48.
 XX PT Novel antisense oligonucleotides useful for inhibiting vascular
 PT endothelial growth factor expression, angiogenesis and for treating
 PT cancer, e.g., Kaposi's sarcoma, ovarian cancer and prostrate cancer -
 XX PS Examples; Fig 14; 105pp; English.
 XX CC The invention provides a composition comprising one or more antisense
 CC oligonucleotides directed against vascular endothelial growth factor
 CC (VEGF) where the antisense oligonucleotides inhibits proliferation of
 CC cells exhibiting autocrine VEGF activity at an IC₅₀ concentration of
 CC between 0.5-2.5 micro M. The antisense oligonucleotides may be directed
 CC against VEGF for inhibiting cancer cell proliferation and angiogenesis.
 CC Preferably the oligonucleotide AAH23032 (a modified version of AAH22984)
 CC is used and may be utilized to treat Kaposi's sarcoma, ovarian cancer,
 CC prostrate cancer, pancreatic cancer or melanoma. The present sequence
 CC represents a VEGF-A gene fragment.
 XX CC
 XX SQ Sequence 62 BP; 12 A; 17 C; 18 G; 15 T; 0 other;

Query Match 100.0%; Score 21; DB 22; Length 62;
 Best Local Similarity 90.5%; Pred. No. 0.89;
 Matches 19; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 UGGCTTGAAGATGACTCGAU 21
 DB 23 TGGCTTGAAGATGACTCGAT 3

RESULT 12
 AAH23005
 ID AAH23005 standard; DNA; 20 BP.
 AC AAH23005;
 DT 17-SEP-2001 (first entry)
 XX VEGF expression inhibiting antisense oligo.
 XX Vascular endothelial growth factor; VEGF; antisense; angiogenesis;
 KW cell proliferation; Kaposi's sarcoma; cancer; melanoma; cytostatic;
 KW antisense therapy; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX WO200152904-A2.
 XX 26-JUL-2001.
 XX 19-JAN-2001; 2001WO-US00019.
 XX 19-JAN-2000; 2000US-0487023.
 XX (GILL/) GILL P S.
 XX Gill PS, Masood R;
 XX WPI; 2001-451898/48.

XX The invention provides a composition comprising one or more antisense
 CC oligonucleotides directed against vascular endothelial growth factor
 CC (VEGF) where the antisense oligonucleotides inhibits proliferation of
 CC cells exhibiting autocrine VEGF activity at an IC₅₀ concentration of
 CC between 0.5-2.5 micro M. The antisense oligonucleotides may be directed
 CC against VEGF for inhibiting cancer cell proliferation and angiogenesis.
 CC Preferably the oligonucleotide AAH23032 (a modified version of AAH22984)
 CC is used and may be utilized to treat Kaposi's sarcoma, ovarian cancer,
 CC prostrate cancer, pancreatic cancer or melanoma. The present sequence
 CC represents a VEGF-A gene fragment.
 XX CC
 XX SQ Sequence 62 BP; 12 A; 17 C; 18 G; 15 T; 0 other;

XX PT Novel antisense oligonucleotides useful for inhibiting vascular
 PT endothelial growth factor expression, angiogenesis and for treating
 PT cancer, e.g., Kaposi's sarcoma, ovarian cancer and prostrate cancer -
 XX PS Claim 10; Page 52; 105pp; English.
 XX CC The invention provides a composition comprising one or more antisense
 CC oligonucleotides directed against vascular endothelial growth factor
 CC (VEGF) where the antisense oligonucleotides inhibits proliferation of
 CC cells exhibiting autocrine VEGF activity at an IC₅₀ concentration of
 CC between 0.5-2.5 micro M. The antisense oligonucleotides may be directed
 CC against VEGF for inhibiting cancer cell proliferation and angiogenesis.
 CC Preferably the oligonucleotide AAH23032 (a modified version of AAH22984)
 CC is used and may be utilized to treat Kaposi's sarcoma, ovarian cancer,
 CC prostrate cancer, pancreatic cancer or melanoma. Sequences AAH22985-23011
 CC represent antisense oligonucleotides directed against VEGF.
 XX SQ Sequence 20 BP; 5 A; 3 C; 6 G; 6 T; 0 other;

Query Match 95.2%; Score 20; DB 22; Length 20;
 Best Local Similarity 95.0%; Pred. No. 2.3;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GGCTTGAAGATGACTCGAU 21
 DB 1 GGCTTGAAGATGACTCGAT 20

RESULT 13
 AAH23008
 ID AAH23008 standard; DNA; 20 BP.
 AC AAH23008;
 DT 17-SEP-2001 (first entry)
 XX VEGF expression inhibiting antisense oligo.
 XX Vascular endothelial growth factor; VEGF; antisense; angiogenesis;
 KW cell proliferation; Kaposi's sarcoma; cancer; melanoma; cytostatic;
 KW antisense therapy; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX WO200152904-A2.
 XX 26-JUL-2001.
 XX 19-JAN-2001; 2001WO-US00019.
 XX 19-JAN-2000; 2000US-0487023.
 XX (GILL/) GILL P S.
 XX Gill PS, Masood R;
 XX WPI; 2001-451898/48.

XX The invention provides a composition comprising one or more antisense
 CC oligonucleotides directed against vascular endothelial growth factor
 CC (VEGF) where the antisense oligonucleotides inhibits proliferation of
 CC cells exhibiting autocrine VEGF activity at an IC₅₀ concentration of
 CC between 0.5-2.5 micro M. The antisense oligonucleotides may be directed
 CC against VEGF for inhibiting cancer cell proliferation and angiogenesis.
 CC Preferably the oligonucleotide AAH23032 (a modified version of AAH22984)
 CC is used and may be utilized to treat Kaposi's sarcoma, ovarian cancer,
 CC prostrate cancer, pancreatic cancer or melanoma. Sequences AAH22985-23011
 CC represent antisense oligonucleotides directed against VEGF.
 XX SQ Sequence 20 BP; 5 A; 3 C; 6 G; 6 T; 0 other;

Query Match 95.2%; Score 20; DB 22; Length 20;
 Best Local Similarity 95.0%; Pred. No. 2.3;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GGCTTGAAGATGACTCGAU 21
 DB 1 GGCTTGAAGATGACTCGAT 20

RESULT 13
 AAH23008
 ID AAH23008 standard; DNA; 20 BP.
 AC AAH23008;
 DT 17-SEP-2001 (first entry)
 XX VEGF expression inhibiting antisense oligo.
 XX Vascular endothelial growth factor; VEGF; antisense; angiogenesis;
 KW cell proliferation; Kaposi's sarcoma; cancer; melanoma; cytostatic;
 KW antisense therapy; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX WO200152904-A2.
 XX 26-JUL-2001.
 XX 19-JAN-2001; 2001WO-US00019.
 XX 19-JAN-2000; 2000US-0487023.
 XX (GILL/) GILL P S.
 XX Gill PS, Masood R;
 XX WPI; 2001-451898/48.

XX The invention provides a composition comprising one or more antisense
 CC oligonucleotides directed against vascular endothelial growth factor
 CC (VEGF) where the antisense oligonucleotides inhibits proliferation of
 CC cells exhibiting autocrine VEGF activity at an IC₅₀ concentration of
 CC between 0.5-2.5 micro M. The antisense oligonucleotides may be directed
 CC against VEGF for inhibiting cancer cell proliferation and angiogenesis.
 CC Preferably the oligonucleotide AAH23032 (a modified version of AAH22984)
 CC is used and may be utilized to treat Kaposi's sarcoma, ovarian cancer,
 CC prostrate cancer, pancreatic cancer or melanoma. Sequences AAH22985-23011
 CC represent antisense oligonucleotides directed against VEGF.
 XX SQ Sequence 20 BP; 5 A; 3 C; 6 G; 6 T; 0 other;

CC is used and may be utilized to treat Kaposi's sarcoma, ovarian cancer,
 CC prostrate cancer, pancreatic cancer or melanoma. Sequences AAH22985-23011
 CC represent antisense oligonucleotides directed against VEGF.

XX Sequence 20 BP; 5 A; 3 C; 6 G; 6 T; 0 other;

Query Match 95.2%; Score 20; DB 22; Length 21;
 Best Local Similarity 95.0%; Pred. No. 2.3;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGCTTGAAGATGACTCGA 20
 :|||||
 Db 1 TGGCTTGAAGATGACTCGA 20

RESULT 14
 AAH22998
 ID AAH22998 standard; DNA; 21 BP.

XX AC AAH22998;

DT 17-SEP-2001 (first entry)

XX VEGF expression inhibiting antisense oligo.

XX Vascular endothelial growth factor; VEGF; antisense; angiogenesis;
 KW cell proliferation; Kaposi's sarcoma; cancer; melanoma; cytostatic;
 KW antisense therapy; ss.

XX Synthetic.
 OS Homo sapiens.
 XX WO200152904-A2.

PN 26-JUL-2001.

XX 19-JAN-2001; 2001WO-US000019.

XX 19-JAN-2000; 2000US-0487023.

XX (GILL/) GILL P S.

XX Gill PS, Masood R;

XX WPI; 2001-451898/48.

XX Novel antisense oligonucleotides useful for inhibiting vascular
 PT endothelial growth factor expression, angiogenesis and for treating
 PT cancer, e.g., Kaposi's sarcoma, ovarian cancer and prostrate cancer

XX Claim 3; Page 52; 105pp; English.

XX The invention provides a composition comprising one or more antisense
 CC oligonucleotides directed against vascular endothelial growth factor
 CC (VEGF) where the antisense oligonucleotides inhibits proliferation of
 CC cells exhibiting autocrine VEGF activity at an IC₅₀ concentration of
 CC between 0.5-2.5 micro M. The antisense oligonucleotides may be directed
 CC against VEGF for inhibiting cancer cell proliferation and angiogenesis.
 CC Preferably the oligonucleotide AAH23032 (a modified version of AAH22984)
 CC is used and may be utilized to treat Kaposi's sarcoma, ovarian cancer,
 CC prostrate cancer, pancreatic cancer or melanoma. Sequences AAH22985-23011
 CC represent antisense oligonucleotides directed against VEGF.

XX Sequence 21 BP; 6 A; 3 C; 6 G; 6 T; 0 other;

Query Match 95.2%; Score 20; DB 22; Length 21;
 Best Local Similarity 95.0%; Pred. No. 2.3;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGCTTGAAGATGACTCGA 20
 :|||||
 Db 2 TGGCTTGAAGATGACTCGA 21

RESULT 15
 AAH22999
 ID AAH22999 standard; DNA; 21 BP.

XX AC AAH22999;

DT 17-SEP-2001 (first entry)

XX VEGF expression inhibiting antisense oligo.

XX Vascular endothelial growth factor; VEGF; antisense; angiogenesis;
 KW cell proliferation; Kaposi's sarcoma; cancer; melanoma; cytostatic;
 KW antisense therapy; ss.

XX Synthetic.
 OS Homo sapiens.
 XX WO200152904-A2.

XX 26-JUL-2001.

XX 19-JAN-2001; 2001WO-US000019.

XX 19-JAN-2000; 2000US-0487023.

XX (GILL/) GILL P S.

XX Gill PS, Masood R;

XX WPI; 2001-451898/48.

XX Novel antisense oligonucleotides useful for inhibiting vascular
 PT endothelial growth factor expression, angiogenesis and for treating
 PT cancer, e.g., Kaposi's sarcoma, ovarian cancer and prostrate cancer

XX Claim 3; Page 52; 105pp; English.

XX The invention provides a composition comprising one or more antisense
 CC oligonucleotides directed against vascular endothelial growth factor
 CC (VEGF) where the antisense oligonucleotides inhibits proliferation of
 CC cells exhibiting autocrine VEGF activity at an IC₅₀ concentration of
 CC between 0.5-2.5 micro M. The antisense oligonucleotides may be directed
 CC against VEGF for inhibiting cancer cell proliferation and angiogenesis.
 CC Preferably the oligonucleotide AAH23032 (a modified version of AAH22984)
 CC is used and may be utilized to treat Kaposi's sarcoma, ovarian cancer,
 CC prostrate cancer, pancreatic cancer or melanoma. Sequences AAH22985-23011
 CC represent antisense oligonucleotides directed against VEGF.

XX Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 other;

Query Match 95.2%; Score 20; DB 22; Length 21;
 Best Local Similarity 95.0%; Pred. No. 2.3;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCTTGAAGATGACTCGAU 21
 :|||||
 Db 1 GGCTTGAAGATGACTCGAT 20

Search completed: December 23, 2002, 05:43:27
 Job time : 313 secs

us-09-805-761-34.rni

Mon, Dec 23 08:43:29 2002

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: December 23, 2002, 05:30:18 : Search time 71 Seconds
(without alignments)
90.707 Million cell updates/sec

Title: US-09-805-761-34

Perfect score: 21 ugcttgagatgtactcgau 21

Sequence: 1 ugcttgagatgtactcgau 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues 662272

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	DB ID	Description
1	21	100.0	21	4	US-09-016-541-2
2	21	100.0	42	3	US-08-765-340-7
3	20	95.2	20	3	US-08-765-340-50
4	15	71.4	20	3	US-08-765-340-51
5	14.8	70.5	24	4	US-09-643-597-355
6	14.8	70.5	27	3	US-08-567-200A-42
7	14.8	70.5	27	3	US-08-691-794-45
8	14	66.7	20	3	US-08-765-340-49
9	13.8	65.7	73	4	US-09-044-796A-6
10	13.8	65.7	73	4	US-09-725-460A-6
11	13.6	64.8	31	3	US-09-032-894-109
12	13.6	64.8	31	3	US-09-031-626-109
13	13.6	64.8	31	4	US-08-679-645-267
14	13.6	64.8	45	3	US-09-164-023-22
15	13.6	64.8	68	4	US-08-483-511-48
16	13.6	64.8	68	5	PCT-US93-01009-48
17	13.6	64.8	20	4	US-09-851-520-44
18	13.6	64.8	20	4	US-08-480-552-21
19	13.2	62.9	20	1	US-08-929-208-21
20	13.2	62.9	20	3	US-09-568-315-21
21	13.2	62.9	20	3	US-09-032-894-108
22	13.2	62.9	21	3	US-09-032-894-112
23	13.2	62.9	21	4	US-09-031-626-108
24	13.2	62.9	21	4	US-09-031-626-112
25	13.2	62.9	24	3	US-08-567-200A-13
26	13.2	62.9	24	3	US-08-691-794-16
27	13.2	62.9	33	4	US-09-252-292-7

28	13.2	62.9	39	1	US-08-456-840-11	Sequence 11, Appl
29	13.2	62.9	39	1	US-08-266-407A-11	Sequence 11, Appl
30	13.2	62.9	39	2	US-08-892-544-11	Sequence 11, Appl
31	13	61.9	14	3	US-08-765-340-138	Sequence 138, Appl
32	12.8	61.0	29	4	US-09-121-539-4	Sequence 4, Appl
33	12.8	61.0	29	4	US-09-121-539-5	Sequence 5, Appl
34	12.8	61.0	30	1	US-08-608-584-23	Sequence 23, Appl
35	12.6	60.0	26	4	US-08-640-737-10	Sequence 10, Appl
36	12.6	60.0	39	1	US-08-014-723-7	Sequence 7, Appl
37	12.6	60.0	39	1	US-08-110-011A-7	Sequence 7, Appl
38	12.6	60.0	49	1	US-08-014-723-8	Sequence 8, Appl
39	12.6	60.0	49	1	US-08-110-011A-8	Sequence 8, Appl
40	12.6	60.0	49	1	US-08-307-444A-11	Sequence 11, Appl
41	12.6	60.0	49	1	US-08-307-444A-13	Sequence 13, Appl
42	12.6	60.0	49	1	US-08-587-389-11	Sequence 11, Appl
43	12.6	60.0	49	1	US-08-587-389-13	Sequence 13, Appl
44	12.6	60.0	51	1	US-08-319-621A-4	Sequence 4, Appl
45	12.6	60.0	53	1	US-08-307-444A-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-09-016-541-2

Sequence 2, Application US/09016541

Patent No. 6291667

GENERAL INFORMATION:

APPLICANT: Gill, Parkesh

APPLICANT: Masood, Rizwan

TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF

TITLE OF INVENTION: KAPOSI'S SARCOMA

FILE REFERENCE: 21327-701

CURRENT APPLICATION NUMBER: US/09/016.541

CURRENT FILING DATE: 1998-01-01

EARLIER APPLICATION NUMBER: US 60/037,004

EARLIER FILING DATE: 1997-01-31

NUMBER OF SEQ ID NOS: 2

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2

LENGTH: 21

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense oligonucleotide to a naturally occurring

OTHER INFORMATION: sequence

US-09-016-541-2

Query Match 100.0%; Score 21; DB 4; Length 21;

Best Local Similarity 90.5%; Pred. No. 0.05;

Matches 19; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGCTTGAAGATGTACTCGAU 21

DB 1 TGGCTTGAAGATGTACTCGAT 21

RESULT 2

US-08-765-340-7/c

Sequence 7, Application US/08765340

Patent No. 6150092

GENERAL INFORMATION:

APPLICANT: UCHIDA, K.

APPLICANT: UCHIDA, T.

APPLICANT: TANAKA, Y.

APPLICANT: MATSUDA, Y.

APPLICANT: KONDO, S.

TITLE OF INVENTION: AN ANTISENSE NUCLEIC ACID

TITLE OF INVENTION: COMPOUND

NUMBER OF SEQUENCES: 185

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

STREET: 345 PARK AVENUE

;; CITY: NEW YORK
;; STATE: NEW YORK
;; COUNTRY: USA
;; ZIP: 10154
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/765,340
;; FILING DATE: 23-DEC-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 145146/94
;; FILING DATE: 27-JUN-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 311130/94
;; FILING DATE: 21-NOV-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: SERUNIAN, LESLIE
;; REGISTRATION NUMBER: 35,353
;; REFERENCE/DOCKET NUMBER: 1452-4005
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 751-6849
;; TELEFAX: (212) 751-6849
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 42 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cdna to mRNA
US-08-765-340-7

Query Match 100.0%; Score 21; DB 3; Length 42;
Best Local Similarity 90.5%; Pred. No. 0.056; 0; Indels 0; Gaps 0;
Matches 19; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 UGGCTTGAAGATGACTCGAU 21
Db :|||||

RESULT 3
US-08-765-340-50
; Sequence 50, Application US/08765340
; Patent No. 6150092
; GENERAL INFORMATION:
; APPLICANT: UCHIDA, K.,
; APPLICANT: UCHIDA, T.,
; APPLICANT: TANAKA, Y.,
; APPLICANT: MATSUDA, Y.,
; APPLICANT: KONDO, S.,
; TITLE OF INVENTION: AN ANTISENSE NUCLEIC ACID
; NUMBER OF SEQUENCES: 185
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,340
; FILING DATE: 23-DEC-1996

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 145146/94
;; FILING DATE: 27-JUN-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 311130/94
;; FILING DATE: 21-NOV-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: SERUNIAN, LESLIE
;; REGISTRATION NUMBER: 35,353
;; REFERENCE/DOCKET NUMBER: 1452-4005
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 751-6849
;; TELEFAX: (212) 751-6849
;; INFORMATION FOR SEQ ID NO: 50:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: Other nucleic acid
;; DESCRIPTION: /desc = "synthetic DNA"
US-08-765-340-50

Query Match 95.2%; Score 20; DB 3; Length 20;
Best Local Similarity 95.0%; Pred. No. 0.16; 0; Indels 0; Gaps 0;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGCTTGAAGATGACTCGAU 21
Db :|||||

RESULT 4
US-08-765-340-51
; Sequence 51, Application US/08765340
; Patent No. 6150092
; GENERAL INFORMATION:
; APPLICANT: UCHIDA, K.,
; APPLICANT: UCHIDA, T.,
; APPLICANT: TANAKA, Y.,
; APPLICANT: MATSUDA, Y.,
; APPLICANT: KONDO, S.,
; TITLE OF INVENTION: AN ANTISENSE NUCLEIC ACID
; NUMBER OF SEQUENCES: 185
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,340
; FILING DATE: 23-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 145146/94
; FILING DATE: 27-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 311130/94
; FILING DATE: 21-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SERUNIAN, LESLIE
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 1452-4005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 751-6849

us-09-805-761-34.rni

Mon, Dec 23 08:43:29 2002

TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
US-08-765-340-51

Query Match 71.4%; Score 15; DB 3; Length 20;
Best Local Similarity 93.3%; Pred. No. 53;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGCTTGAAGATGTA 15
DB 6 TGGCTTGAAGATGTA 20

RESULT 5
US-09-643-597-355/c
Sequence 355, Application US/09643597
Patent No. 6426072
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 355
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
US-09-643-597-355

Query Match 70.5%; Score 14.8; DB 4; Length 24;
Best Local Similarity 83.3%; Pred. No. 69;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 UGGCTTGAAGATGTA 18
DB 19 TGGCTTGAAGATGTA 2

RESULT 6
US-08-367-200A-42
Sequence 42, Application US/08567200A
Patent No. 6020473
GENERAL INFORMATION:
APPLICANT: Keyt, Bruce A.
APPLICANT: Nguyen, Francis H.
APPLICANT: Ferrara, Napoleone
TITLE OF INVENTION: Variants of Vascular Endothelial Cell
TITLE OF INVENTION: Growth Factor, Their Uses, and Processes for their
TITLE OF INVENTION: Production
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/691,794
FILING DATE: 02-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/567,200A
FILING DATE: 05-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-62326-1/WHB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
US-08-567-200A-42

Query Match 70.5%; Score 14.8; DB 3; Length 27;
Best Local Similarity 83.3%; Pred. No. 71;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 CTTGAAGATGTACTCGAU 21
DB 1 CTTGAAGATGTAGCGAT 18

RESULT 7
US-08-691-794-45
Sequence 45, Application US/08691794
Patent No. 6057428
GENERAL INFORMATION:
APPLICANT: Keyt, Bruce A.
APPLICANT: Nguyen, Francis H.
APPLICANT: Ferrara, Napoleone
APPLICANT: Cunningham, Brian C.
APPLICANT: Wells, James A.
APPLICANT: Li, Bing
TITLE OF INVENTION: Variants of Vascular Endothelial Cell
TITLE OF INVENTION: Growth Factor, Their Uses, and Processes for their
TITLE OF INVENTION: Production
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/691,794
FILING DATE: 02-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/002,827
FILING DATE: 25-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/567,200
FILING DATE: 05-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-63758/WHI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-691-794-45

Query Match 70.5%; Score 14.8; DB 3; Length 27;
Best Local Similarity 83.3%; Pred. No. 71;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 CTTGAAGATGTACTCGAU 21
Db 1 CTTGAAGATGTAGCGAT 18
|||||

RESULT 8
US-08-765-340-49
Sequence 49, Application US/08765340
Patent No. 6150092
GENERAL INFORMATION:

APPLICANT: UCHIDA, K.,
APPLICANT: UCHIDA, T.,
APPLICANT: TANAKA, Y.,
APPLICANT: MATSUDA, Y.,
APPLICANT: KONDO, S.,
TITLE OF INVENTION: AN ANTISENSE NUCLEIC ACID
NUMBER OF SEQUENCES: 185
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
SOFTWARE: #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,340
FILING DATE: 23-DEC-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 145146/94
FILING DATE: 27-JUN-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 311130/94
FILING DATE: 21-NOV-1994

ATTORNEY/AGENT INFORMATION:
NAME: SERUNIAN, LESLIE
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 1452-4005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6800
TELEFAX: (212) 751-6849

INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
US-08-765-340-49

Query Match 66.7%; Score 14; DB 3; Length 20;
Best Local Similarity 92.9%; Pred. No. 1.7e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 AAGATGTACTCGAU 21
Db 1 AAGATGTACTCGAT 14
|||||

RESULT 9
US-09-044-796A-6
Sequence 6, Application US/09044796A
Patent No. 6154168
GENERAL INFORMATION:
APPLICANT: Gentz, Reiner L.
APPLICANT: Coleman, Timothy A.
TITLE OF INVENTION: Expression Control Sequences
FILE REFERENCE: PV447
CURRENT APPLICATION NUMBER: US/09/044,796A
CURRENT FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 08/941,020
PRIOR FILING DATE: 1997-09-30
PRIOR APPLICATION NUMBER: 09/044,796
PRIOR FILING DATE: 1998-03-20
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 6
LENGTH: 73
TYPE: DNA
ORGANISM: Homo sapiens
US-09-044-796A-6

Query Match 65.7%; Score 13.8; DB 4; Length 73;
Best Local Similarity 88.2%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCCTTGAAGATGTACTC 18
Db 37 GCCTTGAAGATGTACCC 53
|||||

RESULT 10
US-09-725-460A-6
Sequence 6, Application US/09725460A
Patent No. 6420138
GENERAL INFORMATION:

APPLICANT: Geniez et al.
TITLE OF INVENTION: Expression control sequences
FILE REFERENCE: PV447D1
CURRENT APPLICATION NUMBER: US/09/725,460A
CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 09/044,796
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: US 08/941,020
PRIOR FILING DATE: 1997-09-30
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1

SEQ ID NO 6
LENGTH: 73
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: U+D

; TITLE OF INVENTION: Multiplex Genotyping Using Fluorescent Hybridization
; FILE REFERENCE: 7475-61466
; CURRENT APPLICATION NUMBER: US/09/164,023
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-164-023-22

Query Match 64.8%; Score 13.6; DB 3; Length 45;
Best Local Similarity 75.0%; Pred. No. 3.1e+02;
Matches 15; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 UGCGTTGAAGATGCTACTGA 20
Db :||||| | | | | |
42 TGGCTTGAATCTACTGGA 23

RESULT 15
US-08-483-511-48/c
; Sequence 48, Application US/08483511
; Patent No. 6297048
; GENERAL INFORMATION:
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Lee, William T.L.
; APPLICANT: Townsend, Kay
; APPLICANT: O'Dea, Joanne
; TITLE OF INVENTION: HEPATITIS THERAPEUTICS
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,511
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.407C5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 68 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-483-511-48

Query Match 64.8%; Score 13.6; DB 4; Length 68;
Best Local Similarity 75.0%; Pred. No. 3.4e+02;
Matches 15; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 UGCGTTGAAGATGCTACTGA 20
Db :|||| | | | | | | | | | |
29 TGGCCTGAGATGACCTGGA 10

Search completed: December 23, 2002, 07:15:23
Job time : 72 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 23, 2002, 05:27:58 ; Search time 2135 Seconds
(without alignments)
159.300 Million cell updates/sec

Title: US-09-805-761-34

Perfect score: 21

Sequence: 1 uggctgaagatgtactcgau 21

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 218680

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_estli:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.2	67.6	70	9 AI957173	AI957173 ul82h07.x
2	13.6	64.8	50	9 AU102868	AU102868 AU102868
3	13.6	64.8	60	10 AW119912	AW119912 sd54e02.y
4	13.6	64.8	64	9 AA931487	AA931487 om90a02.s
5	13.2	62.9	52	9 AA755193	AA755193 vg62b10.r
6	13	61.9	71	10 AV554482	AV554482 AV554482

7	12.8	61.0	25	17	AZ804962
c	12.8	61.0	75	13	BH308931
c	12.6	60.0	64	17	BH850101
c	12.6	60.0	74	10	AV957775
c	12.4	59.0	21	9	AU256271
c	12.2	58.1	41	14	T17567
c	12.2	58.1	50	9	AU103181
c	12.2	58.1	50	9	AU103182
c	12.2	58.1	50	9	AU103187
c	12.2	58.1	50	9	AU103188
c	12.2	58.1	50	9	AU103193
c	12.2	58.1	50	14	C01080
c	12.2	58.1	53	17	BH418118
c	12.2	58.1	56	13	BF412547
c	12.2	58.1	58	12	BF206095
c	12.2	58.1	61	9	AI156511
c	12.2	58.1	61	17	AL766608
c	12.2	58.1	62	17	AZ800576
c	12.2	58.1	64	10	AW651855
c	12.2	58.1	67	9	AA122950
c	12.2	58.1	67	17	AZ484608
c	12.2	58.1	73	17	AZ811384
c	12.2	58.1	74	9	AA658138
c	12.2	58.1	74	9	AA236089
c	12.2	58.1	32	10	AV835867
c	12.2	57.1	42	12	BE733174
c	12.2	57.1	43	9	AI155417
c	12.2	57.1	43	9	AA530920
c	12.2	57.1	47	17	TA86020
c	12.2	57.1	49	9	AU258228
c	12.2	57.1	55	17	BH225923
c	12.2	57.1	67	9	AA990325
c	12.2	57.1	71	10	BE306519
c	12.2	57.1	73	13	BI973873
c	12.2	57.1	75	17	B42211
c	11.8	56.2	43	17	BH896966
c	11.8	56.2	45	17	BH896994
c	11.8	56.2	46	9	AI790825
c	11.8	56.2	50	17	BH892206

ALIGNMENTS

RESULT 1
AI957173
LOCUS
DEFINITION
IMAGE:2158621 3' similar to TR:Q02393 Q02393 HUMAN PAPILLOMAVIRUS
18 ES CENTRAL SEQUENCE MOTIF PROTEIN 1 ; mRNA sequence.
AI957173
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AI957173 70 bp mRNA linear EST 20-AUG-1999

ul82h07.x1 Sugano mouse embryo meva Mus musculus cDNA clone

IMAGE:2158621 3' similar to TR:Q02393 Q02393 HUMAN PAPILLOMAVIRUS

18 ES CENTRAL SEQUENCE MOTIF PROTEIN 1 ; mRNA sequence.

AI957173 GI:5749882

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 70)

Marta, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person

, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter

, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,

Waterston, R., and Wilson, R.

The WashU-NCI Mouse EST Project 1999

Unpublished (1999)

Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:1001793

Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 1.

FEATURES

source

1..70
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone_lib="IMAGE:2158621"
/clone_lib="Sugano mouse embryo mewa"
/dev_stage="embryo, 14 dpc"
/lab_host="DH10B"
/note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAGCTGGC and 3' end primer CGACCTGCAGCTCGACGACA."

BASE COUNT 19 a 18 c 18 g 15 t
ORIGIN
Query Match 67.6%; Score 14.2; DB 9; Length 70;
Best Local Similarity 78.9%; Pred. No. 1.3e+04;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 3 GCTTGAAGATGCTACTCGAU 21
||| ||||| |||
Db 44 GCCTGTAGATGTACAGAT 62

RESULT 2

AU102868/c

LOCUS

AU102868 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
COL01564, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Suzuki.Y., Taira.H., Tsunoda.T., Mizushima-Sugano.J., Sese,J., Hata
H., Ota,T., Isogai.T., Tanaka.T., Morishita,S., Okubo,K., Sakaki
Y., Nakamura.Y., Suyama.A. and Sugano.S.

TITLE

Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites

JOURNAL

MEDLINE

COMMENT

EMBO Rep. 2 (5), 388-393 (2001)
21270072
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki.Y., Yoshitomo-Nakagawa.K., Maruyama.K., Suyama.A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

source

1..50
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="COL01564"
/clone_lib="Sugano Homo sapiens cDNA library"

/note="Differential display comparison of untreated and
dimethylformate treated U937 cells"
BASE COUNT 12 a 17 c 8 g 13 t
ORIGIN

Query Match 64.8%; Score 13.6; DB 9; Length 50;
Best Local Similarity 75.0%; Pred. No. 2.3e+04;
Matches 15; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGCTTGAAGATGCTACTCGAU 21

||| ||||| |||

Db 20 GGCTTGAAGATGAATCGCT 1

RESULT 3

AU119912

LOCUS

AU119912
sd54e02.yl Gm-cl016 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-cl016-3603 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE

AUTHORS

1 (bases 1 to 60)
Shoemaker.R., Keim.P., Vodkin.L., Erpelding,J., Corvett.V., Khanna
A., Bolla.B., Marra.M., Hillier.L., Kucaba.T., Martin.J., Beck.C.,
Wylie.T., Underwood.K., Steptoe.M., Theising.B., Allen.M., Bowers
Y., Person.B., Swaller.T., Gibbons.M., Pape.D., Harvey.N., Schurk
R., Ritter.E., Kohn.S., Shin.T., Jackson.Y., Cardenas.M., McCann
R., Waterston.R. and Wilson.R.
Public Soybean EST Project

TITLE

JOURNAL

COMMENT

Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com

Insert Length: 267 Std Error: 0.00

Seq primer: -40RP from Gibco.

FEATURES

source

Location/Qualifiers
1..60

/organism="Glycine max"

/db_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-cl016-3603"

/clone_lib="Gm-cl016"

/tissue_type="Immature flowers of field grown plants"

/lab_host="XL10-Gold"

/note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2:
XhoI; This cDNA library was constructed from mRNA isolated
from immature flowers of field grown plants. The cDNA
library was prepared using the Stratagene pBluescript II
XR library construction kit. Complementary DNA was
synthesized from mRNA using a primer consisting of a poly
(dT) sequence with a XhoI restriction site. EcoRI adapters
were ligated to the blunt-ended cDNA fragments followed by
XhoI digestion. The cDNA fragments were directionally
cloned into the EcoRI-XhoI restriction site of the
pBluescript vector. The ligated cDNA fragments were
transformed into XL10-Gold host cells. This library was
constructed by Dr. Randy Shoemaker and Dr. John
Erpelding."

BASE COUNT

ORIGIN

20 a 8 c 16 g 16 t

ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 1 (bases 1 to 71)
 Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
 A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
 DNA Res. 7, 175-180 (2000)
 20363093
 Contact: Erika Asamizu
 The First Laboratory for Plant Gene Research
 Kazusa DNA Research Institute
 Yana 1532-3, Kisarazu, Chiba 252-0812, Japan
 Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
 FEATURES
 1..71
 /organism="Arabidopsis thaliana"
 /strain="Columbia"
 /db_xref="taxon:3702"
 /clone="R292d12R"
 /clone_lib="Arabidopsis thaliana roots Columbia"
 /tissue_type="roots"
 /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI"
 BASE COUNT 14 a 16 c 14 g 27 t
 ORIGIN
 Query Match 61.9%; Score 13; DB 10; Length 71;
 Best Local Similarity 66.7%; Pred. No. 4.8e+04;
 Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 1 UGCGTTGAAGATGCTACTCGAU 21
 :||| ||||| || |||||
 Db 49 TGGCGTGAAGTCTTCTTGAT 69
 RESULT 7
 AZ804962
 LOCUS 25 bp DNA linear GSS 20-FEB-2001
 DEFINITION 2M0066E10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0066E10 F, DNA sequence.
 ACCESSION AZ804962
 VERSION AZ804962.1 GI:12965773
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 25)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, R., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0066 row: E column: 10
 Seq primer: CTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 25.
 Location/Qualifiers
 1..25
 source

/organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0066E10"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42hv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gii473211419bIAFI29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 BASE COUNT 7 a 4 c 4 g 10 t
 ORIGIN
 Query Match 61.0%; Score 12.8; DB 17; Length 25;
 Best Local Similarity 87.5%; Pred. No. 4.3e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 GCTTGAAGATGCTACTC 18
 ||||| ||||| |||||
 Db 3 GCTTGAAGATGCTACTC 18
 RESULT 8
 BM308931/c
 LOCUS 75 bp mRNA linear EST 02-JAN-2002
 DEFINITION sak52d10.y1 Gm-cl036 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-cl036-6692 5', mRNA sequence.
 ACCESSION BM308931
 VERSION BM308931.1 GI:18040646
 KEYWORDS EST.
 SOURCE soybean.
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 1 (bases 1 to 75)
 Shoemaker, R., Kelm, P., Vodkin, L., Erpelting, J., Corvett, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Willson, R.
 Public Soybean EST Project
 Unpublished (1999)
 Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact: ccu@resgen.com web site: www.resgen.com
 Seq primer: -40RP from Gibco

High quality sequence stop: 70.
Location/Qualifiers
1. .75

FEATURES

source

/organism="Glycine max"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1036-6692"
/clone_lib="Gm-c1036"
/tissue_type="somatic embryos cultured on MSD 20"
/lab_host="DH10B"
/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; This

cDNA library was constructed from mRNA isolated from somatic embryos (age ranging from 2 months to 9 months) cultured on MSD 20. The library was prepared using the Life Technologies pSuperScript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly (dT) sequence with a NotI restriction site. SalI linkers adapted were ligated to the blunt-ended cDNA fragments followed by NotI digestion. The cDNA fragments were directionally cloned into the NotI-SalI restriction site of the pSPORT1 vector. The ligated cDNA fragments were transformed into E.coli Electromax DH10B host cells. This library was constructed in the laboratory of Dr. Lila Vodkin by Anu Khanna at the University of Illinois at Urbana-Champaign. e-mail: l-vodkin@uiuc.edu"

BASE COUNT 20 a 20 c 15 g 20 t

ORIGIN

Query Match 61.0%; Score 12.8; DB 13; Length 75;
Best Local Similarity 81.2%; Pred. No. 6.1e+04;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 TGAAGATGCTACTCGAU 21

DB 35 TGAAGATGCGCTCGAT 20

RESULT 9

BH850101/c

LOCUS BH850101 64 bp DNA linear GSS 13-JUN-2002
DEFINITION SALK_070808.52.35.x Arabidopsis thaliana TONA insertion lines
Arabidopsis thaliana genomic clone SALK_070808.52.35.x, DNA sequence.

ACCESSION BH850101.1 GI:21420972

VERSION GSS.

KEYWORDS thale cress.

SOURCE Arabidopsis thaliana

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 64)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TONA.

Class: TONA tagged.

Location/Qualifiers

1. .64

/organism="Arabidopsis thaliana"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SALK_070808.52.35.x"

BASE COUNT 18 a 14 c 11 g 21 t

ORIGIN

Query Match 60.0%; Score 12.6; DB 17; Length 64;
Best Local Similarity 78.9%; Pred. No. 7.2e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GCCTTGAAGATGCTACTCGA 20

DB 26 GCCTTTAAATGAACCTGA 8

RESULT 10

AV957775/c

LOCUS AV957775 74 bp mRNA linear EST 14-MAR-2002

DEFINITION AV957775 Nori Satoh unpublished cDNA library, egg Clona

intestinalis cDNA clone cie05111 5', mRNA sequence.

ACCESSION AV957775

VERSION AV957775.1 GI:19446074

KEYWORDS EST.

SOURCE Ciona intestinalis.

ORGANISM Ciona intestinalis

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

Phlebobranchia; Clonidae; Clona.

1 (bases 1 to 74)

Satoh,N., Satou,Y., Kohara,Y. and Shin-I,T.

Expressed genes in Ciona intestinalis

Unpublished (2000)

Contact: Nori Satoh

Department of zoology

Kyoto University

Sakyo-Ku, Kyoto, Kyoto 606-8502, Japan

Tel: 81-75-753-4081

Fax: 81-75-703-1113

Email: satoh@scidian.zool.kyoto-u.ac.jp.

Location/Qualifiers

1. .74

/organism="Ciona intestinalis"

/db_xref="taxon:7719"

/clone="cie05111"

/clone_lib="Nori Satoh unpublished cDNA library, egg"

/tissue_type="whole animal"

/dev_stage="egg"

/note="Vector: pBluescript SK"

BASE COUNT 24 a 15 c 17 g 18 t

ORIGIN

Query Match 60.0%; Score 12.6; DB 10; Length 74;
Best Local Similarity 73.7%; Pred. No. 7.5e+04;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 GCCTTGAAGATGCTACTCGAU 21

DB 66 GCCTGGAGATGCTACTTGCT 48

RESULT 11

AU256271/c

LOCUS AU256271 21 bp mRNA linear EST 25-APR-2002

DEFINITION AU256271 3'-directed mouse cDNA library Mus musculus cDNA clone

BED0007940 3', mRNA sequence.

ACCESSION AU256271

VERSION AU256271.1 GI:20319799

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
 AUTHORS Kato,K. and Matoba,R.
 TITLE Generation of expressed sequence tags from mouse brain
 JOURNAL Unpublished (2002)
 COMMENT

Contact: Kikuya Kato
 Graduate School of Biological Sciences
 Nara Institute of Science and Technology
 8916-5 Takayama, Ikoma, Nara 630-0101, Japan
 Tel: 81-743-72-5581
 Fax: 81-743-72-5589
 Email: kkatob@is.nara.ac.jp
 URL: http://love2.alist-nara.ac.jp/BED/index.html.

FEATURES

source

1. .21
 Location/Qualifiers
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="BED0007940"
 /clone_lib="3'-directed mouse cDNA library"
 /tissue_type="brain"
 /note="Vector: pGEN-T-easy"
 8 a 7 c 2 g 4 t

BASE COUNT
 ORIGIN

Query Match 59.0%; Score 12.4; DB 9; Length 21;
 Best Local Similarity 85.7%; Pred. No. 6.2e+04;
 Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DGGCTTGAAGATCT 14

Db 19 TGGCTTGAAGAGGT 6

RESULT 12

T17567/c

LOCUS T17567 41 bp mRNA linear EST 06-JUN-1994
 DEFINITION mps v288 the blue guys library Saccharomyces cerevisiae cDNA sequence upstream of LacZ fusion similar to RNR2, M17221, mRNA sequence.

ACCESSION T17567.1

VERSION 1 GI:458589

KEYWORDS EST

SOURCE baker's yeast.

ORGANISM Saccharomyces cerevisiae

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 41)

Roeder,G.S. and Snyder,M.
 Burns,N., Grinwade,B., Ross-Macdonald,P.B., Choi,E.-Y., Finberg,K., Large-scale analysis of gene expression, protein localization and gene disruption in Saccharomyces cerevisiae

Genes Dev. 8, 1087-1105 (1994)

95011603

Contact: Snyder M

Department of Biology

Yale University

New Haven CT 06520-8103

Tel: 2034326139

Fax: 2034326161

Email: snymic@alevm.ycc.yale.edu

LacZ fusion; Vegetative expression; Beta-gal fusion localization pattern: diffuse cytoplasmic; Disruption phenotype: inviable, large budded arrest; Fusion: codon 222 of RNR2 gene. Sequence below near or adjacent to lacZ.

Seq primer: LacZ sequences in transposon.

Location/Qualifiers

1. .41

/organism="Saccharomyces cerevisiae"

/db_xref="taxon:4932"

/clone_lib="The blue guys library"

/lab_host="E.coli"

/note="Vector: pRECmtn; A yeast genomic DNA library was

FEATURES

source

Qy 3 GCTTGAAGATGACTCG 19
 Db 49 GCTTGAAGATGACTCG 33

Query Match 58.1%; Score 12.2; DB 9; Length 50;

Best Local Similarity 82.4%; Pred. No. 1e+05;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

prepared in the vector pHSS6, and subjected to transposon mutagenesis with mtn3. This mini-transposon carries lacZ sequences that lack an initiation codon; expression of lacZ is only provided by in frame fusion to yeast coding sequence. The yeast genomic DNA carrying the transposon was excised from pHSS6 and transplaced back onto the yeast chromosome. Yeast colonies expressing lacZ were screened for in a color assay. A plasmid containing the genomic DNA/lacZ fusion junction was recovered from each individual yeast colony that expressed lacZ activity. These recovered plasmids comprise "The blue guys library". The fusion junction was then sequenced to identify the expressed ORF upstream of the fusion.

BASE COUNT 9 a 14 c 5 g

ORIGIN

Query Match 58.1%; Score 12.2; DB 14; Length 41;

Best Local Similarity 82.4%; Pred. No. 9.5e+04;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GCTTGAAGATGACTCT 18

Db 17 GCTTGAAGATGACTC 1

RESULT 13

AU103181/c

LOCUS AU103181

DEFINITION AU103181 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone CAS07662, mRNA sequence.

ACCESSION AU103181

VERSION AU103181.1

KEYWORDS EST

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 50)

AUTHORS Suzuki,Y., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata

,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki

,Y., Nakamura,Y., Suyama,A. and Sugano,S.

Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

21270072

COMMENT

Contact: Yutaka Suzuki

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano

,S. Construction and characterization of a full length-enriched and

a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

Source

1. 50

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CAS07662"

/clone_lib="Sugano Homo sapiens cDNA library"

/note="Differential display comparison of untreated and

dimethylfumarate treated U937 cells"

14 a 8 c 17 g 11 t

BASE COUNT

ORIGIN

RESULT 14
AUI03182/c
LOCUS AUI03182 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION CAS12355, mRNA sequence.
ACCESSION AUI03182
VERSION AUI03182.1 GI:13552703
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
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Location/Qualifiers
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CAS12355"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfumarate treated U937 cells"

BASE COUNT 10 a 13 c 12 g 15 t
ORIGIN
Query Match 58.1%; Score 12.2; DB 9; Length 50;
Best Local Similarity 82.4%; Pred. No. 1e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 GCTTGAAGATGCTACTCG 19
||||| | | | |
Db 37 GCTTGACAGGTAATCG 21

Search completed: December 23, 2002, 07:14:01
Job time : 2140 secs

RESULT 15
AUI03187/c
LOCUS AUI03187 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HEP04033, mRNA sequence.
ACCESSION AUI03187
VERSION AUI03187.1 GI:13552708
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp

FEATURES
source
Location/Qualifiers
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CAS12355"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfumarate treated U937 cells"

BASE COUNT 14 a 10 c 14 g 12 t
ORIGIN
Query Match 58.1%; Score 12.2; DB 9; Length 50;
Best Local Similarity 82.4%; Pred. No. 1e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 GCTTGAAGATGCTACTCG 19
||||| | | | |
Db 44 GCTTGACAGGTAATCG 28

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 23, 2002, 05:39:00 ; Search time 67 Seconds
(without alignments)
124.388 Million cell updates/sec

Title: US-09-805-761-34

Perfect score: 21
Sequence: 1 ugcttgaagatgtactcgau 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 356696 seqs, 198428768 residues

Total number of hits satisfying chosen parameters: 203266

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, NA:

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
- 2: /cgn2_6/ptodata/2/pubpna/PCIT_NEW_PUB.seq:
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
- 6: /cgn2_6/ptodata/2/pubpna/PCITUS_PUBCOMB.seq:
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	9	US-09-805-761-2
2	21	100.0	21	9	US-09-805-761-34
3	21	100.0	21	9	US-09-805-761-50
4	21	100.0	33	9	US-09-805-761-28
5	21	100.0	48	10	US-09-795-006A-15
6	21	100.0	62	9	US-09-805-761-30
7	20	95.2	20	9	US-09-805-761-23
8	20	95.2	20	9	US-09-805-761-26
9	20	95.2	21	9	US-09-805-761-16
10	20	95.2	21	9	US-09-805-761-17
11	19.4	92.4	21	9	US-09-805-761-49
12	19	90.5	19	9	US-09-805-761-24
13	19	90.5	19	9	US-09-805-761-27
14	19	90.5	21	9	US-09-805-761-15
15	19	90.5	21	9	US-09-805-761-18
16	18.4	87.6	21	9	US-09-805-761-55
17	18	85.7	18	9	US-09-805-761-25
18	18	85.7	21	9	US-09-805-761-14
19	18	85.7	21	9	US-09-805-761-19

20	17.8	84.8	21	9	US-09-805-761-48	Sequence 48, Appl
21	17	81.0	20	9	US-09-805-761-20	Sequence 20, Appl
22	16	76.2	19	9	US-09-805-761-21	Sequence 21, Appl
23	15.4	73.3	21	9	US-09-805-761-13	Sequence 13, Appl
24	15.2	72.4	22	10	US-09-917-265-94	Sequence 94, Appl
25	15	71.4	18	9	US-09-805-761-22	Sequence 22, Appl
26	15	71.4	21	9	US-09-805-761-11	Sequence 11, Appl
27	14.8	70.5	24	10	US-09-735-705-355	Sequence 355, App
28	14.8	70.5	24	10	US-09-850-716A-355	Sequence 355, App
29	14.8	70.5	24	10	US-09-897-778-355	Sequence 355, App
30	14.4	68.6	21	9	US-09-805-761-12	Sequence 12, Appl
31	14	66.7	21	9	US-09-805-761-10	Sequence 10, Appl
32	13.6	64.8	68	9	US-09-466-035-48	Sequence 48, Appl
33	13.6	64.8	68	10	US-09-912-679-48	Sequence 48, Appl
34	13.4	63.8	24	10	US-09-997-664-48	Sequence 48, Appl
35	13.2	62.9	32	10	US-09-915-181A-10	Sequence 10, Appl
36	13	61.9	15	10	US-09-365-029-87	Sequence 87, Appl
37	13	61.9	16	10	US-09-365-029-5	Sequence 5, Appl
38	13	61.9	16	10	US-09-365-029-11	Sequence 11, Appl
39	13	61.9	21	9	US-09-805-761-9	Sequence 9, Appl
40	12.8	61.0	29	10	US-09-852-000-4	Sequence 4, Appl
41	12.8	61.0	29	10	US-09-852-000-5	Sequence 5, Appl
42	12.2	58.1	26	9	US-10-055-364-21	Sequence 21, Appl
43	12.2	58.1	31	10	US-09-801-274-639	Sequence 639, App
44	12.2	58.1	31	10	US-09-801-274-1246	Sequence 1246, Ap
45	12	57.1	12	9	US-09-835-371-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-09-805-761-2
; Sequence 2, Application US/09805761
; Patent No. US20020165174A1
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkesh
; APPLICANT: Masood, Rizwan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTISENSE
; TITLE OF INVENTION: VEGF OLIGONUCLEOTIDES
; FILE REFERENCE: 21327-701CON2
; CURRENT APPLICATION NUMBER: US/09/805,761
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: PCT/US01/00019
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 09/487,023
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 09/016,541
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: US 09/016,541
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/037,004
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2

LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VEGF antisense oligonucleotide
US-09-805-761-2

Query Match 100.0%; Score 21; DB 9; Length 21;
Best Local Similarity 90.5%; Pred. No. 0.047;
Matches 19; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGCTTGAAGATGTACTCGAU 21

Db 1 TGGCTTGAAGATGTACTCGAT 21

RESULT 2

US-09-805-761-34
; Sequence 34, Application US/09805761
; Patent No. US20020165174A1
; GENERAL INFORMATION:
; APPLICANT: Masood, Rizwan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTISENSE
; FILE REFERENCE: 21327-701CON2
; CURRENT APPLICATION NUMBER: US/09/805,761
; PRIOR FILING DATE: 2001-03-13
; PRIOR FILING DATE: 2001-01-19
; PRIOR FILING DATE: 2000-01-19
; PRIOR FILING DATE: 2000-11-24
; PRIOR FILING DATE: 2000-11-24
; PRIOR FILING DATE: 1998-01-30
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mixed backbone oligonucleotides, nucleotides 1-4
US-09-805-761-34

Query Match 100.0%; Score 21; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 UGGCTTGAAGATGTACTCGAU 21
Db 1 UGGCTTGAAGATGTACTCGAU 21

RESULT 3
US-09-805-761-50/c
; Sequence 50, Application US/09805761
; Patent No. US20020165174A1
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkesh
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTISENSE
; FILE REFERENCE: 21327-701CON2
; CURRENT APPLICATION NUMBER: US/09/805,761
; PRIOR FILING DATE: 2001-03-13
; PRIOR FILING DATE: 2001-01-19
; PRIOR FILING DATE: 2000-01-19
; PRIOR FILING DATE: 2000-11-24
; PRIOR FILING DATE: 2000-11-24
; PRIOR FILING DATE: 1998-01-30
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(21)
; OTHER INFORMATION: VEGF-A

US-09-805-761-50

Query Match 100.0%; Score 21; DB 9; Length 21;
Best Local Similarity 90.5%; Pred. No. 0.047;
Matches 19; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 UGGCTTGAAGATGTACTCGAU 21
Db 21 TGGCTTGAAGATGTACTCGAT 1

RESULT 4
US-09-805-761-28
; Sequence 28, Application US/09805761
; Patent No. US20020165174A1
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkesh
; APPLICANT: Masood, Rizwan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTISENSE
; FILE REFERENCE: 21327-701CON2
; CURRENT APPLICATION NUMBER: US/09/805,761
; PRIOR FILING DATE: 2001-03-13
; PRIOR FILING DATE: 2001-01-19
; PRIOR FILING DATE: 2000-01-19
; PRIOR FILING DATE: 2000-11-24
; PRIOR FILING DATE: 2000-11-24
; PRIOR FILING DATE: 1998-01-30
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VEGF antisense oligonucleotide
US-09-805-761-28

Query Match 100.0%; Score 21; DB 9; Length 33;
Best Local Similarity 90.5%; Pred. No. 0.052;
Matches 19; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 UGGCTTGAAGATGTACTCGAU 21
Db 13 TGGCTTGAAGATGTACTCGAT 33

RESULT 5
US-09-795-006A-15
; Sequence 15, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; PRIOR FILING DATE: 2001-02-26
; PRIOR FILING DATE: 2000-05-18
; PRIOR FILING DATE: 2000-05-18
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Artificial chimeric
OTHER INFORMATION: Oligonucleotide sequence derived from multiple vertebrate vascula
OTHER INFORMATION: endothelial growth factor
US-09-795-006A-15

Query Match 100.0%; Score 21; DB 10; Length 48;
Best Local Similarity 90.5%; Pred. No. 0.056;
Matches 19; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 UGGCTTGAAGATGTACTCGAU 21
Db 1 TGGCTTGAAGATGTACTCGAT 21

RESULT 6
US-09-805-761-30/c
Sequence 30, Application US/09805761
Patent No. US20020165174A1
GENERAL INFORMATION:
APPLICANT: Gill, Parkesh
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTISENSE
FILE REFERENCE: 21327-701CON2
CURRENT APPLICATION NUMBER: US/09/805,761
CURRENT FILING DATE: 2001-03-13
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 09/487,023
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 09/016,541
PRIOR FILING DATE: 2000-11-24
PRIOR APPLICATION NUMBER: US 09/016,541
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: US 60/037,004
PRIOR FILING DATE: 1997-01-31
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30
LENGTH: 62
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (3)...(62)
OTHER INFORMATION: VEGF-A
US-09-805-761-30

Query Match 100.0%; Score 21; DB 9; Length 62;
Best Local Similarity 90.5%; Pred. No. 0.059;
Matches 19; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGCTTGAAGATGTACTCGAU 21
Db 23 TGGCTTGAAGATGTACTCGAT 3

RESULT 7
US-09-805-761-23
Sequence 23, Application US/09805761
Patent No. US20020165174A1
GENERAL INFORMATION:
APPLICANT: Gill, Parkesh
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTISENSE
FILE REFERENCE: 21327-701CON2
CURRENT APPLICATION NUMBER: US/09/805,761
CURRENT FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: PCT/US01/00019
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 09/487,023

PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 09/016,541
PRIOR FILING DATE: 2000-11-24
PRIOR APPLICATION NUMBER: US 09/016,541
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: US 60/037,004
PRIOR FILING DATE: 1997-01-31
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VEGF antisense oligonucleotide
US-09-805-761-23

Query Match 95.2%; Score 20; DB 9; Length 20;
Best Local Similarity 95.0%; Pred. No. 0.15;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCTTGAAGATGTACTCGAU 21
Db 1 GGCTTGAAGATGTACTCGAT 20

RESULT 8
US-09-805-761-26
Sequence 26, Application US/09805761
Patent No. US20020165174A1
GENERAL INFORMATION:
APPLICANT: Masood, Rizwan
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTISENSE
FILE REFERENCE: 21327-701CON2
CURRENT APPLICATION NUMBER: US/09/805,761
CURRENT FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: PCT/US01/00019
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 09/487,023
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 09/016,541
PRIOR FILING DATE: 2000-11-24
PRIOR APPLICATION NUMBER: US 09/016,541
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: US 60/037,004
PRIOR FILING DATE: 1997-01-31
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VEGF antisense oligonucleotide
US-09-805-761-26

Query Match 95.2%; Score 20; DB 9; Length 20;
Best Local Similarity 95.0%; Pred. No. 0.15;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGCTTGAAGATGTACTCGA 20
Db 1 TGGCTTGAAGATGTACTCGA 20

RESULT 9
US-09-805-761-16
Sequence 16, Application US/09805761
Patent No. US20020165174A1
GENERAL INFORMATION:
APPLICANT: Gill, Parkesh

APPLICANT: Masood, Rizwan
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTISENSE
FILE REFERENCE: 21327-701CON2
CURRENT APPLICATION NUMBER: US/09/805,761
CURRENT FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: PCT/US01/00019
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 09/487,023
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 09/016,541
PRIOR FILING DATE: 2000-11-24
PRIOR APPLICATION NUMBER: US 09/016,541
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: US 60/037,004
PRIOR FILING DATE: 1997-01-31
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VEGF antisense oligonucleotide
US-09-805-761-16

Query Match 95.2%; Score 20; DB 9; Length 21;
Best Local Similarity 95.0%; Pred. No. 0.16;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UGGCTTGAAGATGTACTCGA 20
Db 2 TGGCTTGAAGATGTACTCGA 21

RESULT 10
US-09-805-761-17
Sequence 17, Application US/09805761
Patent No. US20020165174A1
GENERAL INFORMATION:
APPLICANT: Masood, Rizwan
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTISENSE
FILE REFERENCE: 21327-701CON2
CURRENT APPLICATION NUMBER: US/09/805,761
CURRENT FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: PCT/US01/00019
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 09/487,023
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 09/016,541
PRIOR FILING DATE: 2000-11-24
PRIOR APPLICATION NUMBER: US 09/016,541
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: US 60/037,004
PRIOR FILING DATE: 1997-01-31
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VEGF antisense oligonucleotide
US-09-805-761-17

Query Match 95.2%; Score 20; DB 9; Length 21;
Best Local Similarity 95.0%; Pred. No. 0.16;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGCTTGAAGATGTACTCGAU 21
Db 2 TGGCTTGAAGATGTACTCGAT 21

Db 1 GGCTTGAAGATGTACTCGAT 20

RESULT 11
US-09-805-761-49
Sequence 49, Application US/09805761
Patent No. US20020165174A1
GENERAL INFORMATION:
APPLICANT: Masood, Rizwan
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTISENSE
FILE REFERENCE: 21327-701CON2
CURRENT APPLICATION NUMBER: US/09/805,761
CURRENT FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: PCT/US01/00019
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 09/487,023
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 09/016,541
PRIOR FILING DATE: 2000-11-24
PRIOR APPLICATION NUMBER: US 09/016,541
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: US 60/037,004
PRIOR FILING DATE: 1997-01-31
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 49
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: A mutation of the antisense oligonucleotide SEQ ID
US-09-805-761-49

Query Match 92.4%; Score 19.4; DB 9; Length 21;
Best Local Similarity 85.7%; Pred. No. 0.32;
Matches 18; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 UGGCTTGAAGATGTACTCGAU 21
Db 1 TGGCTTGAAGATGTACTCGAT 21

RESULT 12
US-09-805-761-24
Sequence 24, Application US/09805761
Patent No. US20020165174A1
GENERAL INFORMATION:
APPLICANT: Gill, Parkesh
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTISENSE
FILE REFERENCE: 21327-701CON2
CURRENT APPLICATION NUMBER: US/09/805,761
CURRENT FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: PCT/US01/00019
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 09/487,023
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 09/016,541
PRIOR FILING DATE: 2000-11-24
PRIOR APPLICATION NUMBER: US 09/016,541
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: US 60/037,004
PRIOR FILING DATE: 1997-01-31
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: VEGF antisense oligonucleotide
US-09-805-761-24

Query Match 90.5%; Score 19; DB 9; Length 19;
Best Local Similarity 94.7%; Pred. No. 0.5;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCTTGAAGATGTACTCG 21
:|||||
Db 1 GCTTGAAGATGTACTCGAT 19

RESULT 13

US-09-805-761-27
; Sequence 27, Application US/09805761
; Patent No. US20020165174A1
; GENERAL INFORMATION:
; APPLICANT: Masood, Rizwan
; APPLICANT: Gill, Parkesh
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTISENSE
; FILE REFERENCE: 21327-701CON2
; CURRENT APPLICATION NUMBER: US/09/805,761
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: PCT/US01/00019
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 09/487,023
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 09/016,541
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: US 09/016,541
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/037,004
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VEGF antisense oligonucleotide
US-09-805-761-27

Query Match 90.5%; Score 19; DB 9; Length 19;
Best Local Similarity 94.7%; Pred. No. 0.5;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGCTTGAAGATGTACTCG 19
:|||||
Db 1 TGGCTTGAAGATGTACTCG 19

RESULT 14

US-09-805-761-15
; Sequence 15, Application US/09805761
; Patent No. US20020165174A1
; GENERAL INFORMATION:
; APPLICANT: Masood, Rizwan
; APPLICANT: Gill, Parkesh
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTISENSE
; FILE REFERENCE: 21327-701CON2
; CURRENT APPLICATION NUMBER: US/09/805,761
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: PCT/US01/00019
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 09/487,023
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 09/016,541
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: US 09/016,541

; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/037,004
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VEGF antisense oligonucleotide
US-09-805-761-15

Query Match 90.5%; Score 19; DB 9; Length 21;
Best Local Similarity 94.7%; Pred. No. 0.51;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGCTTGAAGATGTACTCG 19
:|||||
Db 3 TGGCTTGAAGATGTACTCG 21

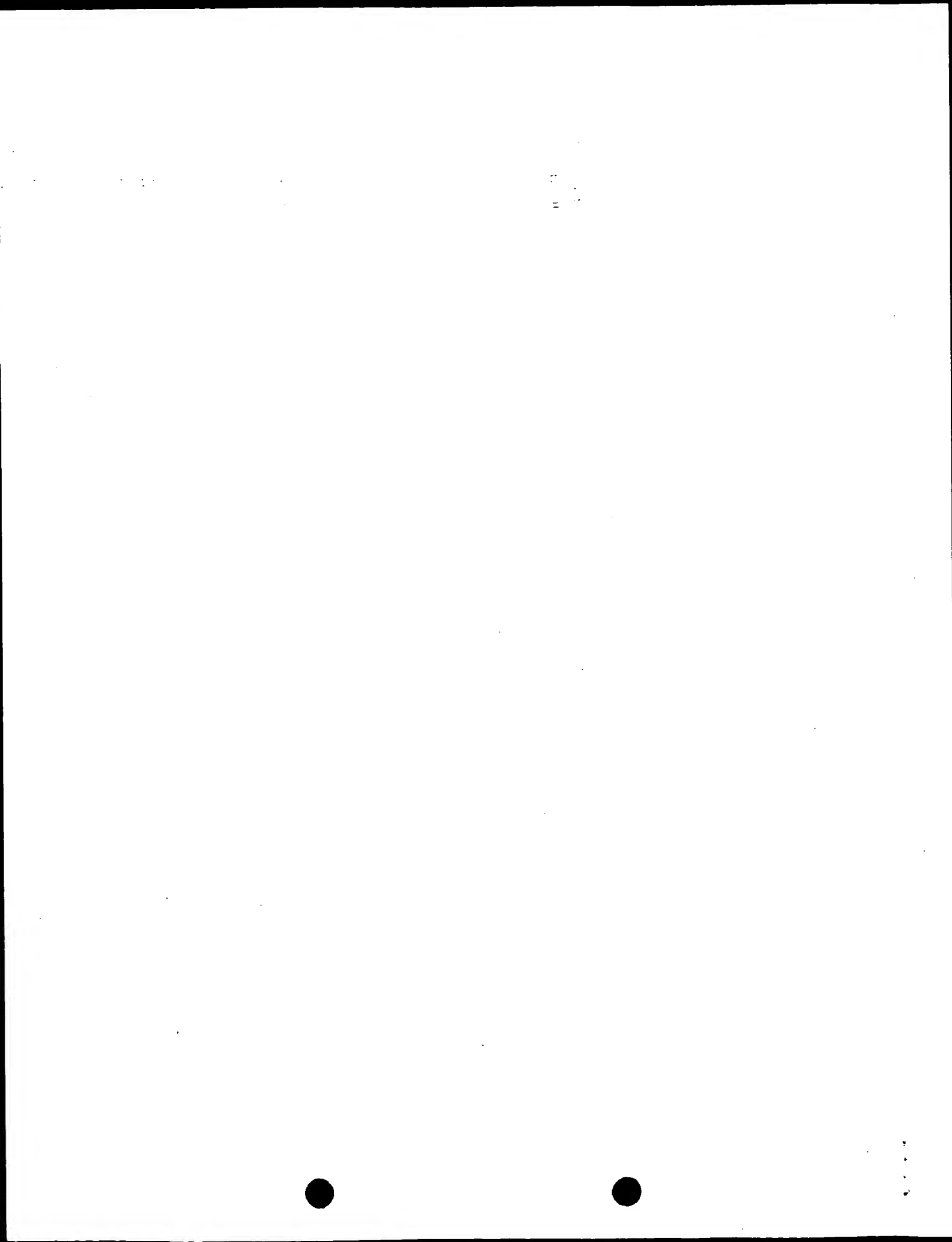
RESULT 15

US-09-805-761-18
; Sequence 18, Application US/09805761
; Patent No. US20020165174A1
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkesh
; APPLICANT: Masood, Rizwan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTISENSE
; FILE REFERENCE: 21327-701CON2
; CURRENT APPLICATION NUMBER: US/09/805,761
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: PCT/US01/00019
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 09/487,023
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 09/016,541
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: US 09/016,541
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/037,004
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VEGF antisense oligonucleotide
US-09-805-761-18

Query Match 90.5%; Score 19; DB 9; Length 21;
Best Local Similarity 94.7%; Pred. No. 0.51;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCTTGAAGATGTACTCG 21
:|||||
Db 1 GCTTGAAGATGTACTCGAT 19

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Job time : 67 secs



GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model
Run on: December 23, 2002, 05:06:49 ; Search time 3267 Seconds
(without alignments)
187.070 Million cell updates/sec

Title: US-09-805-761-34
Perfect score: 21
Sequence: 1 uggttggaagtgtactcgau 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 941340

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 3: gb.in.*
- 4: gb.om.*
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- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	21	100.0	21	6	ARI70717	ARI70717 Sequence
2	21	100.0	21	6	AX203667	AX203667 Sequence
3	21	100.0	21	6	AX203699	AX203699 Sequence
c 4	21	100.0	21	6	AX203715	AX203715 Sequence
5	21	100.0	33	6	AX203693	AX203693 Sequence
c 6	21	100.0	42	6	ARI18881	ARI18881 Sequence
c 7	21	100.0	42	6	E11023	E11023 DNA fragment
8	21	100.0	48	6	AX234365	AX234365 Sequence
c 9	21	100.0	62	6	AX203695	AX203695 Sequence
10	20	95.2	20	6	ARI18924	ARI18924 Sequence
11	20	95.2	20	6	AX203688	AX203688 Sequence
12	20	95.2	20	6	AX203691	AX203691 Sequence
13	20	95.2	21	6	AX203681	AX203681 Sequence
14	20	95.2	21	6	AX203682	AX203682 Sequence
15	19.4	92.4	21	6	AX203714	AX203714 Sequence
16	19	90.5	19	6	AX203689	AX203689 Sequence
17	19	90.5	19	6	AX203692	AX203692 Sequence
18	19	90.5	21	6	AX203680	AX203680 Sequence
19	19	90.5	21	6	AX203683	AX203683 Sequence
c 20	18.4	87.6	21	6	AX203720	AX203720 Sequence
21	18	85.7	18	6	AX203690	AX203690 Sequence
22	18	85.7	21	6	AX203679	AX203679 Sequence
23	18	85.7	21	6	AX203684	AX203684 Sequence
24	17.8	84.8	21	6	AX203713	AX203713 Sequence
25	17	81.0	20	6	AX203685	AX203685 Sequence
26	16	76.2	16	6	AX009101	AX009101 Sequence
c 27	16	76.2	19	6	AX133299	AX133299 Sequence
28	16	76.2	19	6	AX203686	AX203686 Sequence
29	15.4	73.3	21	6	AX203678	AX203678 Sequence
c 30	15.2	72.4	36	6	E91017	E91017 Sequence 14
c 31	15.2	72.4	36	6	E50976	E50976 Assay, rece
32	15	71.4	16	6	AX009100	AX009100 Sequence
33	15	71.4	18	6	AX203687	AX203687 Sequence
34	15	71.4	20	6	ARI18925	ARI18925 Sequence
35	15	71.4	20	6	E14235	E14235 Antisense o
36	15	71.4	21	6	AX203676	AX203676 Sequence
c 37	14.8	70.5	24	6	AX365962	AX365962 Sequence
38	14.4	68.6	21	6	AX203677	AX203677 Sequence
39	14.2	67.6	39	6	AX111382	AX111382 Sequence
40	14	66.7	18	6	AX009121	AX009121 Sequence
41	14	66.7	19	6	AX081924	AX081924 Sequence
c 42	14	66.7	19	6	AX081926	AX081926 Sequence
43	14	66.7	20	6	ARI18923	ARI18923 Sequence
44	14	66.7	21	6	AX203675	AX203675 Sequence
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ALIGNMENTS

RESULT 1
ARI70717
LOCUS ARI70717
DEFINITION Sequence 2 from patent us 6291667.
ACCESSION ARI70717
VERSION ARI70717.1 GI:17908676
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Gill,P.S. and Masood,R.
TITLE Method and composition for treatment of kaposi's sarcoma
JOURNAL Patent: US 6291667-A 2 18-SEP-2001;
FEATURES Location/Qualifiers

ARI70717
21 bp
DNA
linear
PAT 17-DEC-2001

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BASE COUNT 5 a 3 c 6 g 7 t
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Query Match 100.0%; Score 21; DB 6; Length 21;
Best Local Similarity 90.5%; Pred. No. 19;
Matches 19; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGCTTGAAGATGTACTCGAU 21
Db 1 TGGCTTGAAGATGTACTCGAT 21

RESULT 4
AX203715/c
LOCUS AX203715
DEFINITION Sequence 50 from Patent WO0152904.
ACCESSION AX203715
VERSION AX203715.1 GI:15393165
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 21)
AUTHORS Gill, P.S. and Masood, R.
TITLE Methods and compositions for antisense vegf oligonucleotides
JOURNAL Patent: WO 0152904-A 50 26-JUL-2001;
Gill, Parkash, S. (US)
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Location/Qualifiers
/organism="Homo sapiens"
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Best Local Similarity 90.5%; Pred. No. 19;
Matches 19; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGCTTGAAGATGTACTCGAU 21
Db 21 TGGCTTGAAGATGTACTCGAT 1

RESULT 5
AX203693
LOCUS AX203693
DEFINITION Sequence 28 from Patent WO0152904.
ACCESSION AX203693
VERSION AX203693.1 GI:15393135
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 33)
AUTHORS Gill, P.S. and Masood, R.
TITLE Methods and compositions for antisense vegf oligonucleotides
JOURNAL Patent: WO 0152904-A 28 26-JUL-2001;
Gill, Parkash, S. (US)
FEATURES
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Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="VEGF antisense oligonucleotide"
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BASE COUNT 9 a 6 c 11 g 7 t
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Best Local Similarity 90.5%; Pred. No. 19;
Matches 19; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGCTTGAAGATGTACTCGAU 21
Db 1 TGGCTTGAAGATGTACTCGAT 21

source 1. .21
BASE COUNT 5 a 3 c 6 g 7 t
ORIGIN
Query Match 100.0%; Score 21; DB 6; Length 21;
Best Local Similarity 90.5%; Pred. No. 19;
Matches 19; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGCTTGAAGATGTACTCGAU 21
Db 1 TGGCTTGAAGATGTACTCGAT 21

RESULT 2
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LOCUS AX203667
DEFINITION Sequence 2 from Patent WO0152904.
ACCESSION AX203667
VERSION AX203667.1 GI:15393107
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 21)
AUTHORS Gill, P.S. and Masood, R.
TITLE Methods and compositions for antisense vegf oligonucleotides
JOURNAL Patent: WO 0152904-A 2 26-JUL-2001;
Gill, Parkash, S. (US)
FEATURES
source 1. .21
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="VEGF antisense oligonucleotide"
5 a 3 c 6 g 7 t
BASE COUNT 5 a 3 c 6 g 7 t
ORIGIN
Query Match 100.0%; Score 21; DB 6; Length 21;
Best Local Similarity 90.5%; Pred. No. 19;
Matches 19; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGCTTGAAGATGTACTCGAU 21
Db 1 TGGCTTGAAGATGTACTCGAT 21

RESULT 3
AX203699
LOCUS AX203699
DEFINITION Sequence 34 from Patent WO0152904.
ACCESSION AX203699
VERSION AX203699.1 GI:15393145
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 21)
AUTHORS Gill, P.S. and Masood, R.
TITLE Methods and compositions for antisense vegf oligonucleotides
JOURNAL Patent: WO 0152904-A 34 26-JUL-2001;
Gill, Parkash, S. (US)
FEATURES
source 1. .21
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Mixed backbone oligonucleotides, nucleotides 1-4
and 18-21 are 2'O methylriboseosides"
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BASE COUNT 5 a 3 c 6 g 7 t
ORIGIN
Query Match 100.0%; Score 21; DB 6; Length 21;
Best Local Similarity 90.5%; Pred. No. 19;
Matches 19; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Query Match 100.0%; Score 21; DB 6; Length 62;
Best Local Similarity 90.5%; Pred. No. 18;

Matches 19; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGCTTGAAGATGTACTCGAU 21
Db 23 TGGCTTGAAGATGTACTCGAT 3

RESULT 10
AR118924
LOCUS AR118924
DEFINITION Sequence 50 from patent US 6150092.
ACCESSION AR118924
VERSION AR118924.1 GI:14100834
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Uchida,K., Uchida,T., Tanaka,Y., Matsuda,Y. and Kondo,S.
TITLE Antisense nucleic acid compound targeted to VEGF
JOURNAL Patent: US 6150092-A 50 21-NOV-2000;
FEATURES Location/Qualifiers
source
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BASE COUNT 5 a 3 c 6 g 6 t
ORIGIN

Query Match 95.2%; Score 20; DB 6; Length 20;
Best Local Similarity 95.0%; Pred. No. 58;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCTTGAAGATGTACTCGAU 21
Db 1 GGCTTGAAGATGTACTCGAT 20

RESULT 11
AX203688
LOCUS AX203688
DEFINITION Sequence 23 from Patent WO0152904.
ACCESSION AX203688
VERSION AX203688.1 GI:15393130
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Gill,P.S. and Masood,R.
TITLE Methods and compositions for antisense vegf oligonucleotides
JOURNAL Patent: WO 0152904-A 23 26-JUL-2001;
FEATURES Location/Qualifiers
source
1..20
BASE COUNT 5 a 3 c 6 g 6 t
ORIGIN

Query Match 95.2%; Score 20; DB 6; Length 20;
Best Local Similarity 95.0%; Pred. No. 58;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCTTGAAGATGTACTCGAU 21
Db 1 GGCTTGAAGATGTACTCGAT 20

RESULT 12
AX203691
LOCUS AX203691
DEFINITION Sequence 26 from Patent WO0152904.
ACCESSION AX203691

Matches 19; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGCTTGAAGATGTACTCGA 20
Db 2 TGGCTTGAAGATGTACTCGA 21

RESULT 13
AX203681
LOCUS AX203681
DEFINITION Sequence 16 from Patent WO0152904.
ACCESSION AX203681
VERSION AX203681.1 GI:15393122
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 21)
AUTHORS Gill,P.S. and Masood,R.
TITLE Methods and compositions for antisense vegf oligonucleotides
JOURNAL Patent: WO 0152904-A 16 26-JUL-2001;
FEATURES Location/Qualifiers
source
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BASE COUNT 6 a 3 c 6 g 6 t
ORIGIN

Query Match 95.2%; Score 20; DB 6; Length 21;
Best Local Similarity 95.0%; Pred. No. 58;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGCTTGAAGATGTACTCGA 20
Db 2 TGGCTTGAAGATGTACTCGA 21

RESULT 14
AX203682
LOCUS AX203682
DEFINITION Sequence 17 from Patent WO0152904.
ACCESSION AX203682
VERSION AX203682.1 GI:15393123
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 21)
AUTHORS Gill,P.S. and Masood,R.
TITLE Methods and compositions for antisense vegf oligonucleotides
JOURNAL Patent: WO 0152904-A 17 26-JUL-2001;

VERSION AX203691.1 GI:15393133
KEYWORDS synthetic construct.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Gill,P.S. and Masood,R.
TITLE Methods and compositions for antisense vegf oligonucleotides
JOURNAL Patent: WO 0152904-A 26 26-JUL-2001;
FEATURES Location/Qualifiers
source
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BASE COUNT 5 a 3 c 6 g 6 t
ORIGIN

Query Match 95.2%; Score 20; DB 6; Length 20;
Best Local Similarity 95.0%; Pred. No. 58;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGCTTGAAGATGTACTCGA 20
Db 1 TGGCTTGAAGATGTACTCGA 20

RESULT 13
AX203681
LOCUS AX203681
DEFINITION Sequence 16 from Patent WO0152904.
ACCESSION AX203681
VERSION AX203681.1 GI:15393122
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 21)
AUTHORS Gill,P.S. and Masood,R.
TITLE Methods and compositions for antisense vegf oligonucleotides
JOURNAL Patent: WO 0152904-A 16 26-JUL-2001;
FEATURES Location/Qualifiers
source
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BASE COUNT 6 a 3 c 6 g 6 t
ORIGIN

Query Match 95.2%; Score 20; DB 6; Length 21;
Best Local Similarity 95.0%; Pred. No. 58;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGCTTGAAGATGTACTCGA 20
Db 2 TGGCTTGAAGATGTACTCGA 21

RESULT 14
AX203682
LOCUS AX203682
DEFINITION Sequence 17 from Patent WO0152904.
ACCESSION AX203682
VERSION AX203682.1 GI:15393123
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 21)
AUTHORS Gill,P.S. and Masood,R.
TITLE Methods and compositions for antisense vegf oligonucleotides
JOURNAL Patent: WO 0152904-A 17 26-JUL-2001;

FEATURES
 source Gill, Parkash, S. (US)
 1. .21 Location/Qualifiers
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="VEGF antisense oligonucleotide"

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RESULT 15
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 DEFINITION Sequence 49 from Patent WO0152904.
 ACCESSION AX203714
 VERSION AX203714.1 GI:15393163
 KEYWORDS
 SOURCE Synthetic construct.
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Gill, P.S. and Masood, R.
 TITLE Methods and compositions for antisense vegf oligonucleotides
 JOURNAL Patent: WO 0152904-A 49 26-JUL-2001;
 Gill, Parkash, S. (US)

FEATURES
 source Gill, Parkash, S. (US)
 1. .21 Location/Qualifiers
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 /note="A mutation of the antisense oligonucleotide SEQ ID
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Search completed: December 23, 2002, 06:38:09
 Job time : 3269 secs

1. The first part of the document is a list of the names of the persons who were present at the meeting. The names are listed in alphabetical order.

